Package ‘fitmix’

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Title Finite Mixture Model Fitting of Lifespan Datasets

Version 0.1.1

Description Fits the lifespan datasets of biological systems such as yeast, fruit flies, and other similar biological units with well-known finite mixture models introduced by Farewell et al. (1982) <doi:10.2307/2529885> and Al-Hussaini et al. (2000) <doi:10.1080/00949650008812033>. Estimates parameter space fitting of a lifespan dataset with finite mixtures of parametric distributions. Computes the following tasks; 1) Estimates parameter space of the finite mixture model by implementing the expectation maximization (EM) algorithm. 2) Finds a sequence of four goodness-of-fit measures consist of Akaike Information Criterion (AIC), Bayesian Information Criterion (BIC), Kolmogorov-Smirnov (KS), and log-likelihood (log-likelihood) statistics. 3)The initial values is determined by k-means clustering.

URL `https://github.com/guven-code/fitmix/`

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Encoding UTF-8

RoxygenNote 7.1.1.9001

Depends R (>= 3.1.0)

Imports stats

Suggests rmarkdown, knitr

NeedsCompilation no

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Contents

`dmix` *The mixture distribution*

Description

Computing probability density function for the well-known mixture models.

Usage

```
dmix(lifespan, model, K, param)
```

Arguments

`lifespan`	Vector of samples
`model`	choice of one of the mixture models; `gompertz`, `log-logistics`, `log-normal`, and `weibull`.
`K`	number of components
`param`	Vector of weight ω, shape α, and scale β parameters.

Value

A vector of the same length as lifespan data, given the pdf of the one of the mixture models computed at `lifespan`.

Examples

```
lifespan<-seq(0,30,0.2)
K<-2
weight<-c(0.6,0.4)
alpha<-c(0.5,1)
beta<-c(1,0.5)
param<-c(weight,alpha,beta)
dmix(lifespan, "log-logistic", K, param)
```

`fitmixEM` *Fits lifespan data of time units with gompertz, log-logistics, log-normal, and weibull mixture models choice of one.*

Description

Fits lifespan data of time units with gompertz, log-logistics, log-normal, and weibull mixture models choice of one.

Usage

```
fitmixEM(lifespan, model, K, initial = FALSE, starts)
```

Arguments

`lifespan`	numeric vector of lifespan dataset
`model`	model name of the one of the well-known model: `gompertz`,`log-logistics`,`log-normal`, and `weibull`.
`K`	number of well-known model components.
`initial`	logical true or false
`starts`	numeric if initial sets to true

Details

Estimates parameters of the given mixture model implementing the expectation maximization (EM) algorithm. General form for the cdf of a statistical mixture model is given by a distribution f is a mixture of `K component` distributions of $f = (f_1, f_2, ..f_K)$ if

$$f(x) = \sum_{k=1}^{K} \lambda_k f_k(x)$$

with $\lambda_k > 0$, $\sum_k \lambda_k = 1$. This equation is a stochastic model, thus it allows to generate new data points; first picks a distribution of choice, with probablities by weight, then generates another observation according to the chosen distribution. In short represenated by, Z ~ Mult($\lambda_1, \lambda_2, ...\lambda_k$) and X|Z ~ `f_Z`, where `Z` is a discrete random variable which component X is drawn from.

The families considered for the cdf of Gompertz, Log-normal, Log-logistic, and Weibull.

Value

1.The return has three values; the first value is estimate, measures, and cluster.

2. The second value includes four different measurements of goodness-of-fit tests involving: Akaike Information Criterion (`AIC`), Bayesian Information Criterion (`BIC`), Kolmogorov-Smirnov (`KS`), and log-likelihood (`log.likelihood`) statistics.

3. The last value is the output of clustering vector.

References

Farewell, V. (1982). The Use of Mixture Models for the Analysis of Survival Data with Long-Term Survivors. *Biometrics, 38(4), 1041-1046.* doi:10.2307/2529885 McLachlan, G. J. and Peel, D. (2000) *Finite Mixture Models*, John Wiley & Sons, Inc.

Essam K. Al-Hussaini, Gannat R. Al-Dayian & Samia A. Adham (2000) On finite mixture of two-component gompertz lifetime model, *Journal of Statistical Computation and Simulation, 67:1, 20-67*, DOI: 10.1080/00949650008812033

Examples

```
lifespan<-sample(1000)
fitmixEM(lifespan, "weibull", K = 2, initial = FALSE)
```

`pmix` *The mixture cumulative distribution*

Description

Computing cumulative distribution function for the well-known mixture models.

Usage

```
pmix(lifespan, model, K, param)
```

Arguments

`lifespan`	Vector of samples
`model`	choice of one of the mixture models; `gompertz`, `log-logistics`, `log-normal`, and `weibull`.
`K`	number of components
`param`	Vector of weight ω, shape α, and scale β parameters.

Value

A vector of the same length as lifespan data, given the cdf of the one of the mixture models computed at `lifespan`.

Examples

```
lifespan<-seq(0,30,0.2)
K<-2
weight<-c(0.5,0.5)
alpha<-c(0.5,1)
beta<-c(1,0.5)
param<-c(weight,alpha,beta)
pmix(lifespan, "log-logistic", K, param)
```

`rmix` *The mixture random generation for the well-known models*

Description

Random generation for the well-known mixture models with parameters `weigth`, `shape` and `scale`.

Usage

```
rmix(N, model, K, param)
```

Arguments

`N`	Number of inputs for the mixture random generation
`model`	Choice of one of the mixture models; `gompertz`, `log-logistics`, `log-normal`, and `weibull`.
`K`	Number of components
`param`	Vector of weight ω, shape α, and scale β parameters.

Value

Outputs of random generated vector lenght of N from the given mixture model.

Examples

```
N<-100
K<-2
weight<-c(0.5,0.5)
alpha<-c(0.5,1)
beta<-c(1,0.5)
param<-c(weight,alpha,beta)
rmix(N, "weibull", K, param)
```

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